RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/507,446_

Source: _PCT/10_

Date Processed by STIC: _9/23/04_

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PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

PCT

RAW SEQUENCE LISTING   DATE: 09/23/2004
PATENT APPLICATION: US/10/507,446   TIME: 11:50:43

Input Set : A:\Sequence Listing PCT JP0302946.txt
Output Set: N:\CRF4\09232004\J507446.raw

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     3 <110> APPLICANT: GOTO, Hidetsugu
     4        NAKANO, Shigeru
     6 <120> TITLE OF INVENTION: Structural gene responsible for acetic acid resistance in
acetic
     7        acid bacteria, acetic acid bacteria transformed with said gene,
     8        and acetic acid fermentation using said transformations
    10 <130> FILE REFERENCE: 4439-4024
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/507,446
C--> 13 <141> CURRENT FILING DATE: 2004-09-13
    15 <150> PRIOR APPLICATION NUMBER: PCT/JP03/02946
    16 <151> PRIOR FILING DATE: 2003-03-12
    18 <160> NUMBER OF SEQ ID NOS: 10
    20 <170> SOFTWARE: PatentIn version 3.2
    22 <210> SEQ ID NO: 1
    23 <211> LENGTH: 2016
    24 <212> TYPE: DNA
    25 <213> ORGANISM: Gluconacetobacter entanii
    27 <400> SEQUENCE: 1
    28 gatatcaatg gcagcagcaa gatcgttgag gatctggcct ttgattcact ggccgtcatg      60
    30 aattttgtca tggaaatcga ggacacgctc gacgtttccg tgccgcttga ccggctggct     120
    32 gatatccgca ccattgatga tctggctgcc tgtatcgtct ctctcaagca ggcatcctga     180
    34 tacaccatgt cgattttctc gaaatatgaa ggccttgcgt ccgccctgtc ggcggtaacg     240
    36 gccgatggtg ggcgcaaccc gttcaacgtc gtgatcgaaa agcccatttc ctccacggtc     300
    38 gggctgatcg aagggcgcga gacgcttctg ttcggcacca acaactatct tgggctgagc     360
    40 cagtccccgg ccgcgatcga agcggcggtg gaagccgcca gggcttatgg tgtcggcacg     420
    42 accggatcgc gcatcgccaa tggcacgcag ggtctgcacc gccagttgga agagcggctg     480
    44 tgcaccttct tccgtcgtcg gcactgcatg gtgttttcca ccggttacca ggccaatctg     540
    46 ggcacgattt ccgcactggc gggcaaggac gattatctgc tgcttgatgc ggacagccat     600
    48 gccagcatct atgatggcag ccgccttggc catgcgcagg tcatccgctt ccgtcacaac     660
    50 gacgccgatg acctgcataa acgcctgcgc cgccttgatg gtacgcccgg agcgaaactg     720
    52 gtcgtggtcg aaggcatcta ttccatgatg ggcgacgtcg ttcccatggc ggaattcgcg     780
    54 gccgtcaagc gggaaaccgg tgcatggctg ctggcggatg aagcacattc cgttggtgta     840
    56 atgggcgaac atggccgtgg cgtggcggaa tccgacggcg tggaagatga tgtcgatttt     900
    58 gtcgtcggca cctttttccaa aagccttggc acggttggtg ctactgtgt ttccaaccat     960
    60 gccgggctgg acctgatccg gctgtgttcg cgtccgtaca tgttcaccgc atccctgccg    1020
    62 ccggaagtca tcgccgcgac catggccgcg ctgactgaac tggaaaaccg gccggaactg    1080
    64 cgcgtgcggt tgatggacaa tgcacgcagg cttcatgacg ggctgcaggc ggccggcctg    1140
    66 cgcaccggcc cgcaggccag tcctgtcgtg tccgtcattc tggatgatgt ggcggttgcc    1200
    68 gtggcgttct ggaaccggct gctggacctt ggggtttacg tcaacctcag cctgccgcct    1260
    70 gcaacgcccg accagcatcc cctgctgcgg acctccgtca tggcgaccca tacgccggag    1320
    72 cagatagacc gggccgtgga aatcttcgcc gttgtagcgg gcgagatggg tatcaaccgc    1380
    74 gccgcctgaa aaaacctgcc tgccgtaatt tccacagcag atacggcagg cagaccagcg    1440
    76 gatgccgttc cgaaaacggc cccagcggca gttcaatgcc ggaatgccgc ctgatcttcc    1500
    78 atgcgatata gcgcgcgcca ccttcaaacg tgaaggcccc cttgaacagg cggctgacat    1560
```

Does Not Comply
Corrected Diskette Needed

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80 tcagcacgcg ccccagccga ccacgcagcc accagccttc gtacatcttc cggcgcagtt   1620
82 caggtgtcag ctggggggtt agttgatcgc cctcagaccg gaacggcagg ccatcggcgc   1680
84 gccatacatc cggcagcagg cgcctgtacc gtgcttcctg cccctgtagc aggctacgcg   1740
86 gcctgcggcc gttctccaca cgcagttccg caccgtaagt atgggcgaac agggccagcc   1800
88 agtagtcatc ggccgtgccc tgtgccggac ccagggcggc agcccagcgc cccgcctgcc   1860
90 ccaccgcgcg gataatgcag gccaggatgg catcggccgc gtccggttcc ctgacccata   1920
92 caagccgcac aggctggcag aagcgtgccc agaccgtggt atccaacgtg gcgcgtcccg   1980
94 tcatgcggcg gaactgcgct atggacagga tggcca                             2016
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97 <210> SEQ ID NO: 2
98 <211> LENGTH: 400
99 <212> TYPE: PRT
100 <213> ORGANISM: Gluconacetobacter entanii
102 <400> SEQUENCE: 2

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109             20                  25                  30
112 Pro Ile Ser Ser Thr Val Gly Leu Ile Glu Gly Arg Glu Thr Leu Leu
113             35                  40                  45
116 Phe Gly Thr Asn Asn Tyr Leu Gly Leu Ser Gln Ser Pro Ala Ala Ile
117         50                  55                  60
120 Glu Ala Ala Val Glu Ala Ala Arg Ala Tyr Gly Val Gly Thr Thr Gly
121 65                  70                  75                  80
124 Ser Arg Ile Ala Asn Gly Thr Gln Gly Leu His Arg Gln Leu Glu Glu
125             85                  90                  95
128 Arg Leu Cys Thr Phe Phe Arg Arg Arg His Cys Met Val Phe Ser Thr
129             100                 105                 110
132 Gly Tyr Gln Ala Asn Leu Gly Thr Ile Ser Ala Leu Ala Gly Lys Asp
133         115                 120                 125
136 Asp Tyr Leu Leu Leu Asp Ala Asp Ser His Ala Ser Ile Tyr Asp Gly
137     130                 135                 140
140 Ser Arg Leu Gly His Ala Gln Val Ile Arg Phe Arg His Asn Asp Ala
141 145                 150                 155                 160
144 Asp Asp Leu His Lys Arg Leu Arg Arg Leu Asp Gly Thr Pro Gly Ala
145             165                 170                 175
148 Lys Leu Val Val Val Glu Gly Ile Tyr Ser Met Met Gly Asp Val Val
149             180                 185                 190
152 Pro Met Ala Glu Phe Ala Ala Val Lys Arg Glu Thr Gly Ala Trp Leu
153         195                 200                 205
156 Leu Ala Asp Glu Ala His Ser Val Gly Val Met Gly Glu His Gly Arg
157     210                 215                 220
160 Gly Val Ala Glu Ser Asp Gly Val Glu Asp Asp Val Asp Phe Val Val
161 225                 230                 235                 240
164 Gly Thr Phe Ser Lys Ser Leu Gly Thr Val Gly Gly Tyr Cys Val Ser
165             245                 250                 255
168 Asn His Ala Gly Leu Asp Leu Ile Arg Leu Cys Ser Arg Pro Tyr Met
169             260                 265                 270
172 Phe Thr Ala Ser Leu Pro Pro Glu Val Ile Ala Ala Thr Met Ala Ala
173         275                 280                 285
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/507,446

DATE: 09/23/2004
TIME: 11:50:43

Input Set : A:\Sequence Listing PCT JP0302946.txt
Output Set: N:\CRF4\09232004\J507446.raw

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176 Leu Thr Glu Leu Glu Asn Arg Pro Glu Leu Arg Val Arg Leu Met Asp
177    290                   295               300
180 Asn Ala Arg Arg Leu His Asp Gly Leu Gln Ala Ala Gly Leu Arg Thr
181 305                   310               315                   320
184 Gly Pro Gln Ala Ser Pro Val Val Ser Val Ile Leu Asp Asp Val Ala
185                   325               330               335
188 Val Ala Val Ala Phe Trp Asn Arg Leu Leu Asp Leu Gly Val Tyr Val
189                   340               345               350
192 Asn Leu Ser Leu Pro Pro Ala Thr Pro Asp Gln His Pro Leu Leu Arg
193             355               360               365
196 Thr Ser Val Met Ala Thr His Thr Pro Glu Gln Ile Asp Arg Ala Val
197    370                   375               380
200 Glu Ile Phe Ala Val Val Ala Gly Glu Met Gly Ile Asn Arg Ala Ala
201 385                   390               395                   400
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205 <211> LENGTH: 1360
206 <212> TYPE: DNA
207 <213> ORGANISM: Acetobacter aceti
209 <400> SEQUENCE: 3
210 gaagacagct tggatgtatc tatcccgctc gacaaactgg ctgatatccg aacgattaat    60
212 gaccttgccg cttgcattgt tgctctgaaa aacaaagggt gaggcgtgga tgacatcact   120
214 attttccaaa tttgaaggta cggcaggcgc gctgggttcc gttgtggccg taggcggtcg   180
216 caaccctttt gctgttgtta ttgaaaaacc tgtctcttca actgttggaa ttattgaagg   240
218 tcgggaaacg cttcttttg gcaccaataa ctatttgggg cttagtcaat ccaaaaatgc   300
220 cattcaagca gcccagcagg ctgccgcggc atgtggcgta ggcacaacgg gctcacgcat   360
222 tgcaaatggc acacaatccc tgcaccgaca gcttgaaaaa gatattgccg cgttttttgg   420
224 tcggcgtgat gccatggttt tttccacggg gtatcaggca aacctcggca ttatttccac   480
226 gctggcaggt aaggatgacc acctgtttct ggatgctgat agccacgcca gtatctatga   540
228 tggcagccgc ctgagtgcag cagaagttat tcgcttccgc cataatgatc cagacaacct   600
230 ttataaacgc cttaaacgca tggatggcac gccaggcgcc aaattgattg tggttgaagg   660
232 catttattcc atgacgggta atgttgcccc gattgcagaa tttgttgctg ttaaaaaaga   720
234 aacaggcgct tacctgctgg tagatgaagc ccattctttt ggcgtgttgg gtcaaaatgg   780
236 gcgtggtgcc gctgaggctg atggcgtgga agctgatgtg gactttgttg tcggcacatt   840
238 ttccaaaagc ttgggcacag ttggcggtta ctgcgtatct gaccatcctg agctggagtt   900
240 tgtgcgctta aactgccggc cctatatgtt tacggcatcg ctaccgccgg aagttattgc   960
242 tgccacaacg gctgccttga aagatatgca ggcacatcct gaattgcgta agcagcttat  1020
244 ggcaaacgcg cagcaactac atgcaggttt tgtagatatt gggctaaatg ccagcaaaca  1080
246 cgcaaccccca gttattgccg ttacattgga aacagctgaa gaagctattc ccatgtggaa  1140
248 caggcttttg gaacttggtg tttatgtaaa tctcagcctt cctccggcta caccagattc  1200
250 gcggccgttg ctccgttgtt ccgtaatggc cacccatacg cccgaacaaa ttgcgcaggc  1260
252 tattgccata ttcaggcagg ctgcggcaga agtaggcgta accatcacac cctccgctgc  1320
254 ttaaaaaaaa gctatttgcg cttgaatgcc ccttgctgcc                        1360
257 <210> SEQ ID NO: 4
258 <211> LENGTH: 404
259 <212> TYPE: PRT
260 <213> ORGANISM: Acetobacter aceti
262 <400> SEQUENCE: 4
264 Met Thr Ser Leu Phe Ser Lys Phe Glu Gly Thr Ala Gly Ala Leu Gly
265 1               5                   10                  15
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268 Ser Val Val Ala Val Gly Gly Arg Asn Pro Phe Ala Val Val Ile Glu
269          20              25              30
272 Lys Pro Val Ser Ser Thr Val Gly Ile Ile Glu Gly Arg Glu Thr Leu
273          35              40              45
276 Leu Phe Gly Thr Asn Asn Tyr Leu Gly Leu Ser Gln Ser Lys Asn Ala
277          50              55              60
280 Ile Gln Ala Ala Gln Gln Ala Ala Ala Ala Cys Gly Val Gly Thr Thr
281 65              70              75              80
284 Gly Ser Arg Ile Ala Asn Gly Thr Gln Ser Leu His Arg Gln Leu Glu
285          85              90              95
288 Lys Asp Ile Ala Ala Phe Phe Gly Arg Arg Asp Ala Met Val Phe Ser
289          100             105             110
292 Thr Gly Tyr Gln Ala Asn Leu Gly Ile Ile Ser Thr Leu Ala Gly Lys
293          115             120             125
296 Asp Asp His Leu Phe Leu Asp Ala Asp Ser His Ala Ser Ile Tyr Asp
297          130             135             140
300 Gly Ser Arg Leu Ser Ala Ala Glu Val Ile Arg Phe Arg His Asn Asp
301 145             150             155             160
304 Pro Asp Asn Leu Tyr Lys Arg Leu Lys Arg Met Asp Gly Thr Pro Gly
305          165             170             175
308 Ala Lys Leu Ile Val Val Glu Gly Ile Tyr Ser Met Thr Gly Asn Val
309          180             185             190
312 Ala Pro Ile Ala Glu Phe Val Ala Val Lys Lys Glu Thr Gly Ala Tyr
313          195             200             205
316 Leu Leu Val Asp Glu Ala His Ser Phe Gly Val Leu Gly Gln Asn Gly
317          210             215             220
320 Arg Gly Ala Ala Glu Ala Asp Gly Val Glu Ala Asp Val Asp Phe Val
321 225             230             235             240
324 Val Gly Thr Phe Ser Lys Ser Leu Gly Thr Val Gly Gly Tyr Cys Val
325          245             250             255
328 Ser Asp His Pro Glu Leu Glu Phe Val Arg Leu Asn Cys Arg Pro Tyr
329          260             265             270
332 Met Phe Thr Ala Ser Leu Pro Pro Glu Val Ile Ala Ala Thr Thr Ala
333          275             280             285
336 Ala Leu Lys Asp Met Gln Ala His Pro Glu Leu Arg Lys Gln Leu Met
337          290             295             300
340 Ala Asn Ala Gln Gln Leu His Ala Gly Phe Val Asp Ile Gly Leu Asn
341 305             310             315             320
344 Ala Ser Lys His Ala Thr Pro Val Ile Ala Val Thr Leu Glu Thr Ala
345          325             330             335
348 Glu Glu Ala Ile Pro Met Trp Asn Arg Leu Leu Glu Leu Gly Val Tyr
349          340             345             350
352 Val Asn Leu Ser Leu Pro Pro Ala Thr Pro Asp Ser Arg Pro Leu Leu
353          355             360             365
356 Arg Cys Ser Val Met Ala Thr His Thr Pro Glu Gln Ile Ala Gln Ala
357          370             375             380
360 Ile Ala Ile Phe Arg Gln Ala Ala Ala Glu Val Gly Val Thr Ile Thr
361 385             390             395             400
364 Pro Ser Ala Ala
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RAW SEQUENCE LISTING   DATE: 09/23/2004
PATENT APPLICATION: US/10/507,446   TIME: 11:50:43

Input Set : A:\Sequence Listing PCT JP0302946.txt
Output Set: N:\CRF4\09232004\J507446.raw

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        368 <210> SEQ ID NO: 5          Artificial
        369 <211> LENGTH: 30
        370 <212> TYPE: DNA
C-->    371 <213> ORGANISM: Artifical Sequence      → see p. 6 for error explanation
W-->    373 <220> FEATURE:
W-->    373 <223> OTHER INFORMATION:
W-->    373 <400> 5
        374 ctggctgcct gtatcgtctc tctcaagcag                        30
        377 <210> SEQ ID NO: 6
        378 <211> LENGTH: 30
        379 <212> TYPE: DNA
C-->    380 <213> ORGANISM: Artifical Sequence       same error
W-->    382 <220> FEATURE:
W-->    382 <223> OTHER INFORMATION:
W-->    382 <400> 6
        383 acggctgcag ctggtctgcc tgccgtatct                        30
        386 <210> SEQ ID NO: 7
        387 <211> LENGTH: 30
        388 <212> TYPE: DNA
C-->    389 <213> ORGANISM: Artifical Sequence
W-->    391 <220> FEATURE:
W-->    391 <223> OTHER INFORMATION:
W-->    391 <400> 7
        392 ggcaaacctc ggcattattt ccacgctggc                        30
        395 <210> SEQ ID NO: 8
        396 <211> LENGTH: 29
        397 <212> TYPE: DNA
C-->    398 <213> ORGANISM: Artifical Sequence
W-->    400 <220> FEATURE:
W-->    400 <223> OTHER INFORMATION:
W-->    400 <400> 8
        401 gcgaatctgg tgtagccgga ggaaggctg                         29
        404 <210> SEQ ID NO: 9
        405 <211> LENGTH: 30
        406 <212> TYPE: DNA
C-->    407 <213> ORGANISM: Artifical Sequence
W-->    409 <220> FEATURE:
W-->    409 <223> OTHER INFORMATION:
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        413 <210> SEQ ID NO: 10
        414 <211> LENGTH: 29
        415 <212> TYPE: DNA
C-->    416 <213> ORGANISM: Artifical Sequence
W-->    418 <220> FEATURE:
W-->    418 <223> OTHER INFORMATION:
W-->    418 <400> 10
        419 cagccttcct ccggctacac cagattcgc                         29
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/23/2004
PATENT APPLICATION: US/10/507,446   TIME: 11:50:44

Input Set : **A:\Sequence Listing PCT JP0302946.txt**

error Explanation Output Set: **N:\CRF4\09232004\J507446.raw**

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:5,6,7,8,9,10

VERIFICATION SUMMARY   DATE: 09/23/2004
PATENT APPLICATION: US/10/507,446   TIME: 11:50:44

Input Set : **A:\Sequence Listing PCT JP0302946.txt**
Output Set: **N:\CRF4\09232004\J507446.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:371 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:373 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:373 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:373 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:373
L:380 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:382 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:382 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:382 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:382
L:389 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:391 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:391 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
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L:391 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:391
L:398 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:400 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:400 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:400 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:400
L:407 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:409 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>
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L:409 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
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L:409 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:409
L:416 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:418 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:418 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:418 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:418